

Amendments to the Specification

A. Please replace the Title with the following:

**Genetic Constructs Recombinant Expression Cassettes Having Heterologous 3'
Polyadenylation Signal Sequence Motifs That Function In Plants**

B. Please replace the paragraph on page 15-16 with the following:

The BLAST and BLAST 2.0 algorithms are described in Altschul et al., Nuc. Acids Res., 25:3389-3402 (1977) and Altschul et al., J. Mol. Biol., 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a word length (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff, Proc. Natl. Acad. Sci. USA, 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

C. Please replace the Abstract with the following:

The present invention relates to heterologous genes comprising non-plant 3' termination sequences and plant expression cassettes incorporating the heterologous genes provides recombinant expression cassettes comprising a non-plant 3' termination sequence which is functional in a plant. The recombinant expression cassettes comprise a plant promoter operably linked to a coding sequence having a stop codon, and the non-plant 3' termination sequence. The non-plant 3' termination sequence is heterologous to the coding sequence. The non-plant 3' termination sequence comprises structural features including a cleavage site, a positioning element, and an upstream element. The present invention also comprises methods for construction of the plant expression cassettes and introducing the cassettes into plant cells.